

1 GTCGACCCACGCGTCCGCAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGT 60
 1 M D Q S T Q A C A G 10
 61 GAGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGG 120
 11 E K H C H N R G G L H F R M L P L Q T W 30
 121 CACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACCTTGCCCAGCAACTCTTATTCA 180
 31 H V C R Q A G L L F L Q T L P S N S Y S 50
 181 AATAAAGGAGAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 240
 51 N K G E T S C H Q C D P D K Y S E K G S 70
 241 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 300
 71 ~~S S C~~ N V R P A C T D K D Y F Y T H T A 90
 301 TGCGATGCCAACGGAGAGACACAACCTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 360
 91 C D A N G E T Q L M Y K W A K P K I C S 110
 361 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 420
 111 E D L E G A V K L P A S G V K T H C P P 130
 421 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 480
 131 C N P G F F K T N N S T C Q P C P Y G S 150
 481 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 540
 151 Y S N G S D C T R C P A G T E P A V G F 170
 541 GAATACAAATGGTGAACACGCTGCCCACAAACATGGAACGACCGTTCTCAGTGGGATC 600
 171 E Y K W W N T L P T N M E T T V L S G I 190
 601 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGCTGATCACATTTACACAGCT 660

FIG.1A

191 N F E Y K G M T G W E V A G D H I Y T A 210
 661 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTAGACCT 720
 211 A ~~G A S D N D~~ F M I L T L V V P G F R P 230
 721 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTGTCTTT 780
 231 P Q S V M A D T E N K E V A R I T F V F 250
 781 GAGACCCTCTGTTCTGTGAAGTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 840
 251 E T L C S V N C E L Y F M V G V N S R T 270
 841 AACACTCCTGTGGAGACGTGGAAGGTCCAAAGGCAAACAGTCCTATACCTACATCATT 900
 271 N T P V E T W K G S K G K Q S Y T Y I I 290
 901 GAGGAGAACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 960
 291 E E N T T T S F T W A F Q R T T F H E A 310

 961 AGCAGGAAGTACACCAATGACCTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1020
 311 S R K Y T N D V A K I Y S I N V T N V M 330
 1021 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1080
 331 N G V A S Y C R P C A L E A S D V G S S 350
 1081 TGCACCTCTTGTCTGCTGGTTACTATATTGACCGAGATTGAGAACCTGCCACTCCTGC 1140
 351 C T S C P A G Y Y I D R D S G T C H S C 370
 1141 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1200
 371 P P N T I L K A H Q P Y G V Q A C V P C 390
 1201 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 1260
 391 G P G T K N N K I H S L C Y N D C T F S 410

FIG.1B

1261 CGCAACACTCCAACCAGGACTTTCAACTACAACCTCTCCGCTTTGGCAAACACCGTCACT 1320
 411 R N T P T R T F N Y N F S A L A N T V T 430

1321 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 1380
 431 L A G G P S F T S K G L K Y F H H F T L 450

1381 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 1440
 451 S L C G N Q G R K M S V C T D N V T D L 470

1441 CGGATTCCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 1500
 471 R I P E G E S G F S K S I T A Y V C Q A 490

1501 GTCATCATCCCCCAGAGGTGACAGGCTACAAGCCGGGGTTTCCTCACAGCCTGTCAGC 1560
 491 V I I P P E V T G Y K A G V S S Q P V S 510

1561 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 1620
 511 L A D R L I G V T T D M T L D G I T S P 530

1621 GCTGAACCTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 1680
 531 A E L F H L E S L G I P D V I F F Y R S 550

1681 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 1740
 551 N D V T Q S C S S G R S T T I R V R C S 570

1741 CCACAGAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 1800
 571 P Q K T V P G S L L L P G T C S D G T C 590

1801 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCCTCTGCTCAGTG 1860
 591 D G C N F H F L W E S A A A C P L C S V 610

1861 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 1920

FIG.1C

611 A D Y H A I V S S C V A ~~G I Q K T~~ T Y V 630
 1921 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTCTCTGCCTGAGCAGAGAGTCACCATC 1980
 631 W R E P K L C S G G I S L P E Q R V T I 650
 1981 TGCAAAACCATAGATTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2040
 651 C K T I D F W L K V ~~G I S A G T C T A I~~ 670
 2041 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAACTAGAGTACAAGTAC 2100
 671 L L T V L T C Y F W K K N Q K L E Y K Y 690
 2101 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2160
 691 S K L V M N A T L K D C D L P A A D S C 710
 2161 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAATCACTCT 2220
 711 A I M E G E D V E D D L I F T S K N H S 730
 2221 TTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTGACTCAGTGCCGC 2280
 731 L G R S N H L P P R G L L M D L T Q C R 750
 2281 TGAAGACATCCTCAGGAGGCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCTG 2340
 751 * 751
 2341 CCTCCTCACCTGCATAGCACCTTTGCAAGCCTGCGGCGATTGGGTGCCAGCATCCTGC 2400
 2401 AACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTCAGATCT 2460
 2461 TTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCCA 2520
 2521 CACTTTGTTGTAAATTAAAAAAAAAAAAAAAAAAAA 2554

FIG.1D

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		10	20	30	
1	M D O S T Q A C A G E K H C H N R G G L H F R M L P L O T W	TR13.aa			
1	M - - - - - C V G A R R - L G R G P - - - - -	gi 472958 OX40 homologue			
		40	50	60	
31	H V C R O A G L L F L O T L P S N S Y S N K G E T S C H O C	TR13.aa			
13	- - C - - A A L L L L - G L G L S T V T G - - - - - L H C	gi 472958 OX40 homologue			
		70	80	90	
61	D P D K Y S E K G S S S C N V R P A C T D K D Y F Y T H T A	TR13.aa			
32	V G D T Y P S N D R C C H E C R P G - - - - -	gi 472958 OX40 homologue			
		100	110	120	
91	C D A N G E T Q L M Y K W A K P K I C S E D L E G A V K L P	TR13.aa			
50	- - - - - N G M V S R C	gi 472958 OX40 homologue			
		130	140	150	
121	A S G V K T H C P P C N P G F F K T N N S T C Q P C P Y G S	TR13.aa			
57	S R S Q N T V C R P C G P G F Y N - D V V S S K P C - - - -	gi 472958 OX40 homologue			
		160	170	180	
151	Y S N G S D C T R C P A G T E P A V G F E Y K W W N T L P T	TR13.aa			
82	- - - - K P C T W C - - - - -	gi 472958 OX40 homologue			
		190	200	210	
181	N M E T T V L S G I N F E Y K G M T G W E V A G D H I Y T A	TR13.aa			
88	- - - - -	gi 472958 OX40 homologue			

FIG. 2A

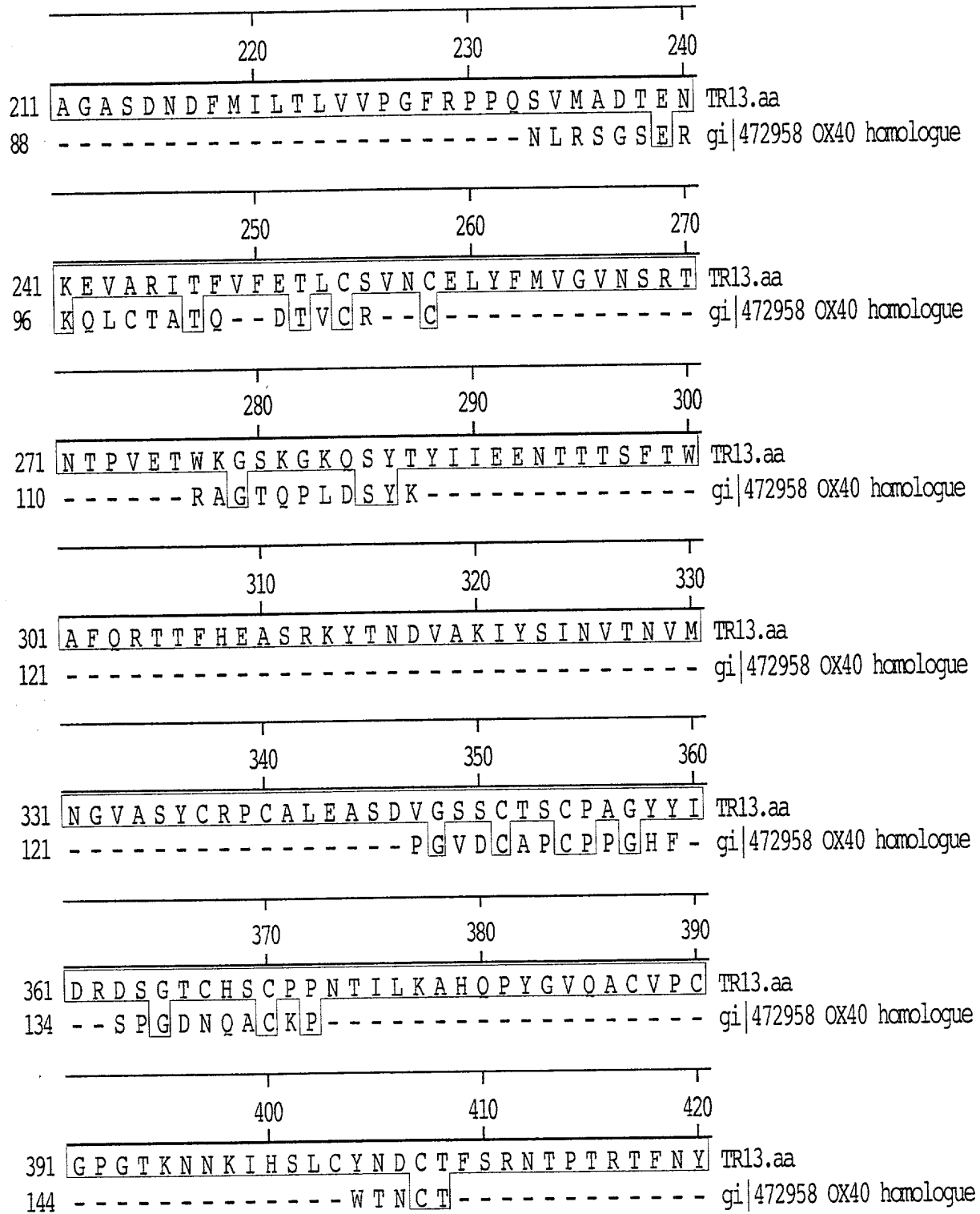


FIG. 2B

	430	440	450	
421	NFSALANTVTLAGGPSFTSKGLKYFHHFTL	TR13.aa		
149	---LAKGKHTLQPASNSSD-----	gi 472958 OX40 homologue		
	460	470	480	
451	SLCGNQGRKMSVCTDNVTDLRIP EGESGF S	TR13.aa		
164	-----AICEDRDPPATQPEQETQG--	gi 472958 OX40 homologue		
	490	500	510	
481	KSITAYVCQAVIIPPEVTGYKAGVSSQPV S	TR13.aa		
182	-----PP-----ARPI T	gi 472958 OX40 homologue		
	520	530	540	
511	LADRLIGVTTDMTLDGITSPAELFHLESLG	TR13.aa		
189	VQ-----PTEA-----	gi 472958 OX40 homologue		
	550	560	570	
541	IPDVIFFYRSNDVTQSCSSGRSTTIRVRC S	TR13.aa		
195	-----	gi 472958 OX40 homologue		
	580	590	600	
571	POKTVPGSLLLPGTCS DGTCDGCNHFHFLWE	TR13.aa		
195	-----WP	gi 472958 OX40 homologue		
	610	620	630	
601	SAAACPLCSVADYHAIVSSCVAGIQKTTYV	TR13.aa		
197	RTSOGP-----	ci 472958 OX40 homologue		

FIG. 2C

		640	650	660	
631	W R E P K L C S G G I S L P E Q R V T I C K T I D F W L K V				TR13.aa
203	- - - - - S T R P V E V P G G R - A V A A I L G L G L V L				gi 472958 OX40 homologue
		670	680	690	
661	G I S A G T C T A I L L T V L T C Y F W K K N Q K L E Y K Y				TR13.aa
226	G L L G P L - - A I L L A L - - - Y L L R R D Q R L P P D A				gi 472958 OX40 homologue
		700	710	720	
691	S K L V M N A T L K D C D L P A A D S C A I M E G E D V E D				TR13.aa
251	H K P P G G G S F R - - - - - T P I Q E E Q A D A				gi 472958 OX40 homologue
		730	740	750	
721	D L I F T S K N H S L G R S N H L P P R G L L M D L T Q C R				TR13.aa
271	H S T L A - - - - - - - - - - - - - - - - - K				gi 472958 OX40 homologue
751					TR13.aa
277	I				gi 472958 OX40 homologue

FIG. 2D

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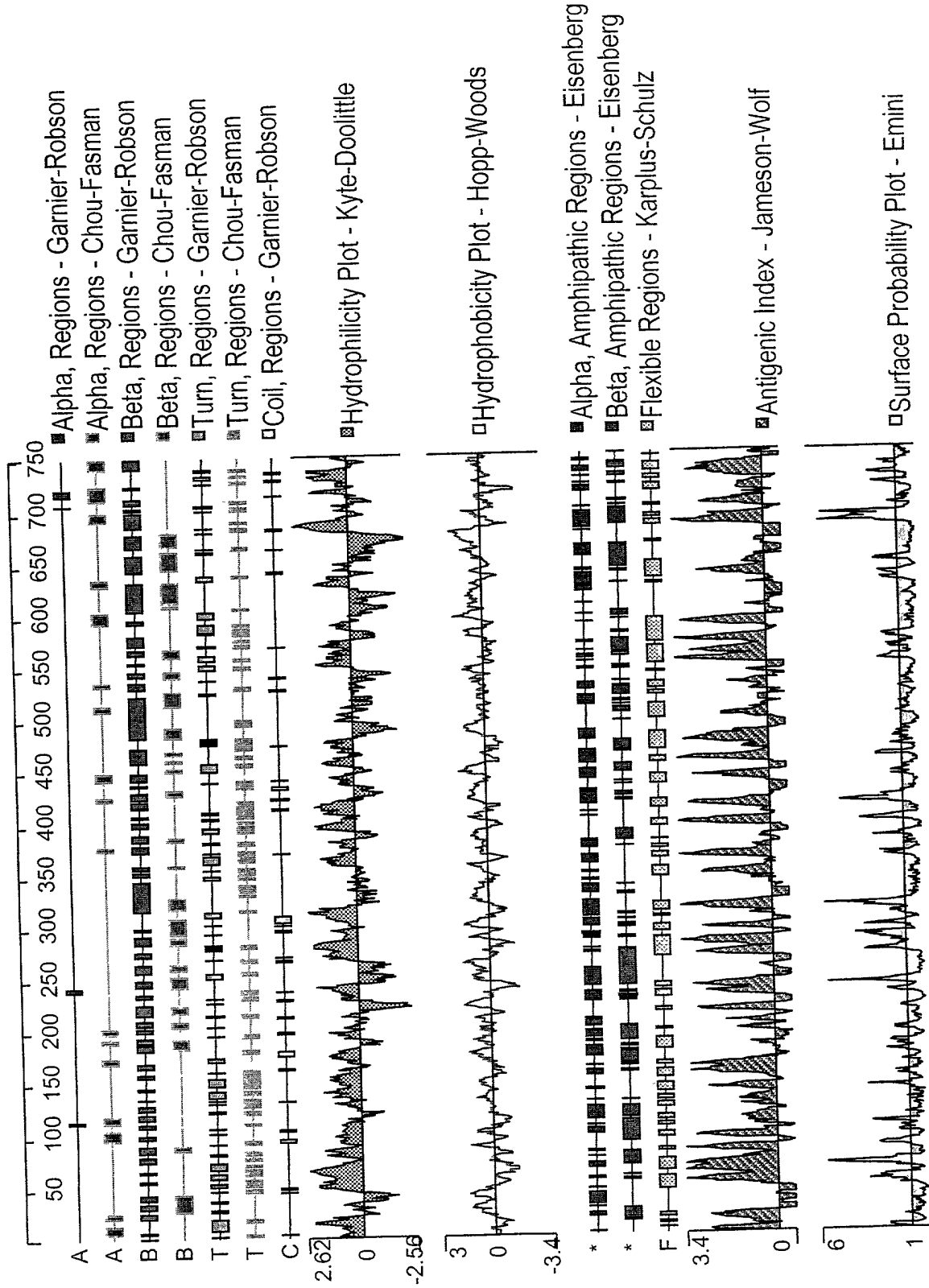


FIG. 3

1 TGAGGTGGATTGTACCGGAGTCCCATTGGGAGCAAGAGCCATCTACTCGTCCGTTACC 60
 61 GGCCTTCCCACCATGGATTGCCAAGAAAATGAGTACTGGGACCAATGGGGACGGTGTGTC 120
 1 M S T G T N C D G V S 11
 121 ACCTGCCAACGGTGTGGTCCCTGGACAGGAGCTATCCAAGGATTGTGGTTATGGAGAGGGT 180
 12 P A N G V V L D R S Y P R I V V M E R V 31
 181 GGAGATGCCTACTGCACAGCCTGCCCTCCTCGCAGTACAAAAGCAGCTGGGGCCACCACA 240
 32 E M P T A Q P A L L A V Q K Q L G P P Q 51
 241 AATGTGCAGAGTTGCATGCACCTGTGCTGTCAATCGTTCAGAAGGTCAACTGCAC 300
 52 M C R V A C T C A V I N R V Q K V N C T 71
 301 ACCTACCTCTAATGCTGTCTGTGGGACTGTTTGCCAGGTTCTACCGAAAGACACGCAT 360
 72 P T S N A V C G D C L P R F Y R K T R I 91
 361 TGGAGGCCTGCAGGACCAAGAGTGCATCCCGTGCACGAAGCAGACCCCCACCTCTGAGGT 420
 92 G G L Q D Q E C I P C T K Q T P T S E V 111
 421 TCAATGTGCCTTCCAGTTGAGCTTAGTGGAGGCAGATGCACCCACAGTGCCCCCTCAGGA 480
 112 Q C A F Q L S L V E A D A P T V P P Q E 131
 481 GGCCACACTTGTTGCACTGGTGAAGCAGCCTGCTAGTGGTGTACCTGGCCTTCCTGGG 540
 132 A T L V A L V S S L L V V F T L A F L g 151
 541 GCTCTTCTCCTCTACTGCAAGCAGTTCTTCAACAGACATTGCCAGCGTGGAGGTTTGCT 600
 152 l f f l y c k q f f n r h c q r g g l l 171

 601 GCAGTTTGAGGCTGATAAAACAGCAAAGGAGGAATCTCTCTTCCCGTGCCACCCAGCAA 660
 172 q f e a d k t a k e e s l f p v p p s k 191

FIG.4A

661 GGAGACCAGTGTCTGAGTCCCAAGTCTCTTGGGCCCCCTGGCAGCCTTGCCCAGTTGTTCTC 720
 192 e t s a e s q v s w a p g s l a q l f s 211
 721 TCTGGACTCTGTTCCCTATACCACAACAGCAGCAGGGCCCTGAAATGTGATGTCCACAAGA 780
 212 l d s v p i p q q q q g p e m * 227
 781 GCTAATACCCTACAGATGGGGCATATCCTATCCCATCCCACCAGAGGATTGATTCTCCAT 840
 841 TTCACAAGGACTGATCTGGAGCATTCTTGCTTCCCTGTTGTAGTCTGGGGAGCCAGATT 900
 901 CCACATTTCATGGGACTACCAGACATGTTCTAGCTCAACTTGATTATAGAGAAGAGGAGA 960
 961 GAGGACAGTGAATGGGGTAGGGTTTTTCATGTCTGCATTTTTGGTCAGGTAAGCCTCTCAA 1020
 1021 AATTGTGTTGGCACATCTACCTAGCACTTTAGGGACAAAATCAAACCCTTCTCCCCTTTT 1080
 1081 AGCTCCTCCCACTGCCTCCCTCCTCAACACACACACACACATACACACACATATACA 1140
 1141 TAGACACACAAACACACACACACACATTAATATCTATCTTGGGGGAAGCCTCGTGCCATA 1200
 1201 ATTCCCAAGTCATGTCTCAGACTGCTGCATTGCAGCATGACGCAGGGCAAACACTTTCCC 1260
 1261 TCTAGATCCCTGGGGCTTACCCTGTATTGAGGTTCTCACCACCCTCAGCAGGGAGAAG 1320
 1321 GGCTGAAGTTCGCCATTTTGGAACTTACAGAACATTTCTGAGCCAAAGTAATCTTCCTT 1380
 1381 CTGGGGCCTGAGTCCCCAACTACCCACAGCAGTCCCTCAAAGACAGCCCTCAATCCA 1440
 1441 TGTAGGGACATCTGAGTATGCCTCTTTCTATTGAAATGTCAATTCAATCCCAGCTTTCTC 1500
 1501 ACCACCGTTCCCCTTTGATTCTTTCTCAATTGTCTTTTTGCCTTTAGCTCCACCTATAC 1560

FIG.4B

1561 ATCTCATGCTCAGAGAAAAACAAGTTCCTTAGAGGTTGTATTCTTTATTCTCCAAGAATC 1620
 1621 TGTCTGAAACTTGTACAGCTAGTTCCTGTCCCACAACCTATTAAGTGGTTTATTAAGTACA 1680
 1681 TTAGGCAGAATGTGCACTTCATCACCAGGTTCTAGCTCTGGCAAAGGAGTGCTGTCTACA 1740
 1741 GCAAGATTTTTGCTTTTAGAATTTTATTAACACATCTTTTGGGTTTCATCCATCTACAAA 1800
 1801 CACTGATTAAGGGCCCCCTGGGGCAACCAATTGATCAGATTACTAAAAGGACTTGGGAAAA 1860
 1861 AGCAAAAAGGTCCCATTGTACTGGACTGAGGATTAGAAGCAATTGAAATACAAGCCTGTA 1920
 1921 CCAAGCAAGCAGCCTGGCCCCACACAGGTATTAGCAAATATGTGGTAACCAAGGTTTTAG 1980
 1981 GCCTTGGCCCCCTAGGTTTCCTGTTTTTTTTTCGTTTTGGTTTCCGTTTTTCGTTTTTGC 2040
 2041 ACAGGTATTCTTATCTCACTGGCTTTCCTGATCATGTTTAGACCTTCTGGTAGAAGAA 2100
 2101 ATAATATCCAGACAGGGGATGATTTGGCTTCAGCAGGCTGCAGGTGTTCAAAGGTTGCCA 2160
 2161 TGTGGCTGGCAGTGGTTCAAGCCACATTTGACACTGCTGCTCTAGAGGAAAGATAATGA 2220
 2221 TGGTAACACAGTAATAATAATAATAACAAAAATATGATAAAGTGAAAGACTAGATTT 2280
 2281 CTTTCAGTGTGCTTGCTCCATGGCATGAATGCTATGTGGACAGCCCAAGCCATACCCAGA 2340
 2341 ATCACCTTAATTCCTAACTTTTTGAGGTTGAGCAATTGGAGGTGGCAATTGGCTTTGCATT 2400
 2401 TTAAAGTATTTGGGTAAAGGTGAAGTGAAGGATTTTCCTCTTTATAATTTCTGTTTGGC 2460
 2461 CATGGCAAATACCATAGTTGAGTATTTGCTTCAGGAGAGTTCTTTTTACAGTTTACTTT 2520

FIG.4C

2521 TCAATGCTGAGGCATATTTCTTTGAGCACTGTGCTTTTATGTGTCTTTCTACAAAGGGGT 2580

2581 TATTGGTCAGTGAAGAACAAGTACACTTGATAAAAACATTTTCAACATACATTGAGCC 2640

2641 TAAACAGCAGTTAAGTTGTCTCTAATGAAGTAGCAAAAAAAAAAATGTAGTTTTTGTTT 2700

2701 GTAAGGAAGGGGAGGTATTTCCCTGAGAATGAATTTTTTTTTTTTGGATTACTGTTTTTC 2760

2761 TCTCCATATACCTTGACTTGGATTTTGACAGGAGGGAGTCTGGGAAAATAATTTTTTCCT 2820

2821 CCAAGATTCTCAGATCCAGGTTAGGAAAGGATTCAGCACTACAGCATACCCCTCTACAAC 2880

2881 ATACAGCCCTGTCACATTGAGATCATAATCCCTCCTGTCCCACTCCTCTCTACCAACCCC 2940

2941 ACCCTACTAGCTAGGTCTTCAGTGTTTTACATTGAATATTGGTACATTTTAATTATTTTT 3000

3001 TCTCATAAATGGGTTATTTATAGAGATTTTGTTAACTCTTGAGCCATATGCATGTGTAGA 3060

3061 TACTGGCAGGCCTATGTTTGTATGATGCTCTGCAAACATTTTATATTGGCCAATAAAC 3120

3121 AGAAATATATCCAAAAAAAAAAAAAAAAAtnTaRmssngsgnatdATGGATTGCCAAGAA 3180

3181 AATGAGTACTGGGACCAATGGGGACGGTGTGTACCTGCCAACGGTGTGGTCTCTGGACAG 3240

3241 GAGCTATCCAAGGATTGTGGTTATGGAGAGGGTGCAGATGCCTACTGCACAGCCTGCCCT 3300

3301 CCTCGCAGTACAAAAGGCAGCTGGGGCCACCACAAATGTCAGAGTTGCATCACCTGTGCT 3360

3361 GTCATCAATCGTGTTCAGAAGGTCAACTGCACAGCTACCTCTAATGCTGTCTGTGGGGAC 3420

3421 TGTTTGCCAGGTTCTACCGAAAGACACGCATTGGAGGCCTGCAGGACCAAGAGTGCATC 3480

FIG.4D

3481 CCGTGCACGAAGCAGACCCCCACCTCTGAGGTTCAATGTGCCTTCCAGTTGAGCTTAGTG 3540
3541 GAGGCAGATGCACCCACAGTGGCCCTCAGGAGGCCACACTTGTTGCACTGGTGAGCAGC 3600
3601 CTGCTAGTGGTGTGTTACCCCTGGCCTTCCTGGGGCTCTTCTTCCTCTACTGCAAGCAGTTC 3660
3661 TTCAACAGACATTGCCAGCGTGGAGGTTTGCTGCAGTTTGAGGCTGATAAAACAGCAAAG 3720
3721 GAGGAATCTCTCTTCCCCGTGCCACCCAGCAAGGAGACCAGTGCTGAGTCCCAAGTCTCT 3780
3781 TGGGCCCCTGGCAGCCTTGCCAGTTGTTCTCTCTGGACTCTGTTCCCTATACCACAACAG 3840
3841 CAGCAGGGGCCTGAAATGTGA 3861

FIG.4E

FIG. 5A

FIG. 5A

	10	20	30																																			
1	M	S	T	G	T	N	G	D	G	V	S	P	A	N	G	V	V	L	D	R	S	Y	P	R	I	V	V	M	E	R	TR14.aa							
1	M	A	P	V	A	-	-	-	-	V	W	A	A	L	A	V	G	L	E	L	W	A	A	H	A	L	P	A	Q	gi 339758 Tumor Necrosis Factor								
	40	50	60																																			
31	V	E	M	P	-	-	T	A	O	P	A	L	L	A	V	O	K	O	L	-	-	G	P	P	Q	M	C	R	V	A	TR14.aa							
27	V	A	F	T	P	Y	A	P	E	P	G	S	T	C	R	L	R	E	Y	D	Q	T	A	Q	M	C	C	S	K	gi 339758 Tumor Necrosis Factor								
	70	80	90																																			
57	C	T	C	A	V	I	N	R	V	O	K	V	N	C	T	P	T	S	N	A	V	C	G	D	C	L	P	R	F	Y	TR14.aa							
57	C	S	P	G	-	-	-	Q	H	A	K	V	F	C	T	K	T	S	D	T	V	C	D	S	C	E	D	S	T	Y	gi 339758 Tumor Necrosis Factor							
	100	110	120																																			
87	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TR14.aa							
84	T	Q	L	W	N	W	V	P	E	C	L	S	C	G	S	R	C	S	S	D	Q	V	E	T	Q	A	C	T	R	E	gi 339758 Tumor Necrosis Factor							
	130	140	150																																			
87	-	-	-	-	-	-	-	-	-	R	K	T	R	I	G	G	L	Q	D	Q	E	-	-	-	-	-	-	-	-	-	-	TR14.aa						
114	Q	N	R	I	C	T	C	R	P	G	W	Y	C	A	L	S	K	Q	E	G	C	R	L	C	A	P	L	R	K	C	gi 339758 Tumor Necrosis Factor							
	160	170	180																																			
99	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	I	P	C	T	K	O	T	-	-	-	-	TR14.aa						
144	R	P	G	F	G	V	A	R	P	G	T	E	T	S	D	V	V	C	K	P	C	A	P	G	T	F	S	N	T	T	gi 339758 Tumor Necrosis Factor							
	190	200	210																																			
107	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	T	S	E	V	Q	C	A	-	-	-	TR14.aa							
174	S	S	T	D	I	C	R	P	H	Q	I	C	N	V	V	A	I	P	G	N	A	S	R	D	A	V	C	T	S	T	gi 339758 Tumor Necrosis Factor							
	220	230	240																																			
115	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	F	Q	L	S	L	V	E	A	D	A	P	T	V	P	P	O	E	A	TR14.aa
204	S	P	T	R	S	M	A	P	G	A	V	H	L	P	Q	P	V	S	T	R	S	Q	H	T	Q	P	T	P	E	P	gi 339758 Tumor Necrosis Factor							

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FIG. 5B

133 TLVALVSSLLVV - - - - - FT L A F - TR14.aa
 234 STAPST S F L L P M G P S P P A E G S T G D F A L P V G gi|339758 Tumor Necrosis Factor

150 - - - - - L G L F F L - - - - - Y C K O F F N R H - - - - - C TR14.aa
 264 L I V G V T A L G L L I I G V V N C V I M T Q V K K K P L C gi|339758 Tumor Necrosis Factor

166 - Q R G G L L - Q F E A D K T - - - - - A K E E S L F P V P TR14.aa
 294 L Q R E A K V P H L P A D K A R G T Q G P E Q Q H L L I T A gi|339758 Tumor Necrosis Factor

189 P S K - - - - - TR14.aa
 324 P S S S S S S L E S S A S A L D R R A P T R N Q P Q A P G V gi|339758 Tumor Necrosis Factor

192 - - - - - TR14.aa
 354 E A S G A G E A R A S T G S S D S S P G G H G T Q V N V T C gi|339758 Tumor Necrosis Factor

192 - - - - - TR14.aa
 384 I V N V C S S S D H S S Q C S S Q A S S T M G D T D S S P S gi|339758 Tumor Necrosis Factor

192 E T S A E S Q V S W A - - - - - P G S L A Q L TR14.aa
 414 E S P K D E Q V P F S K E E C A F R S Q L E T P E T L L G S gi|339758 Tumor Necrosis Factor

120 F S L D S V P I P Q Q Q Q G P E M TR14.aa
 444 T E E K P L P L G V P D A G M K P S gi|339758 Tumor Necrosis Factor

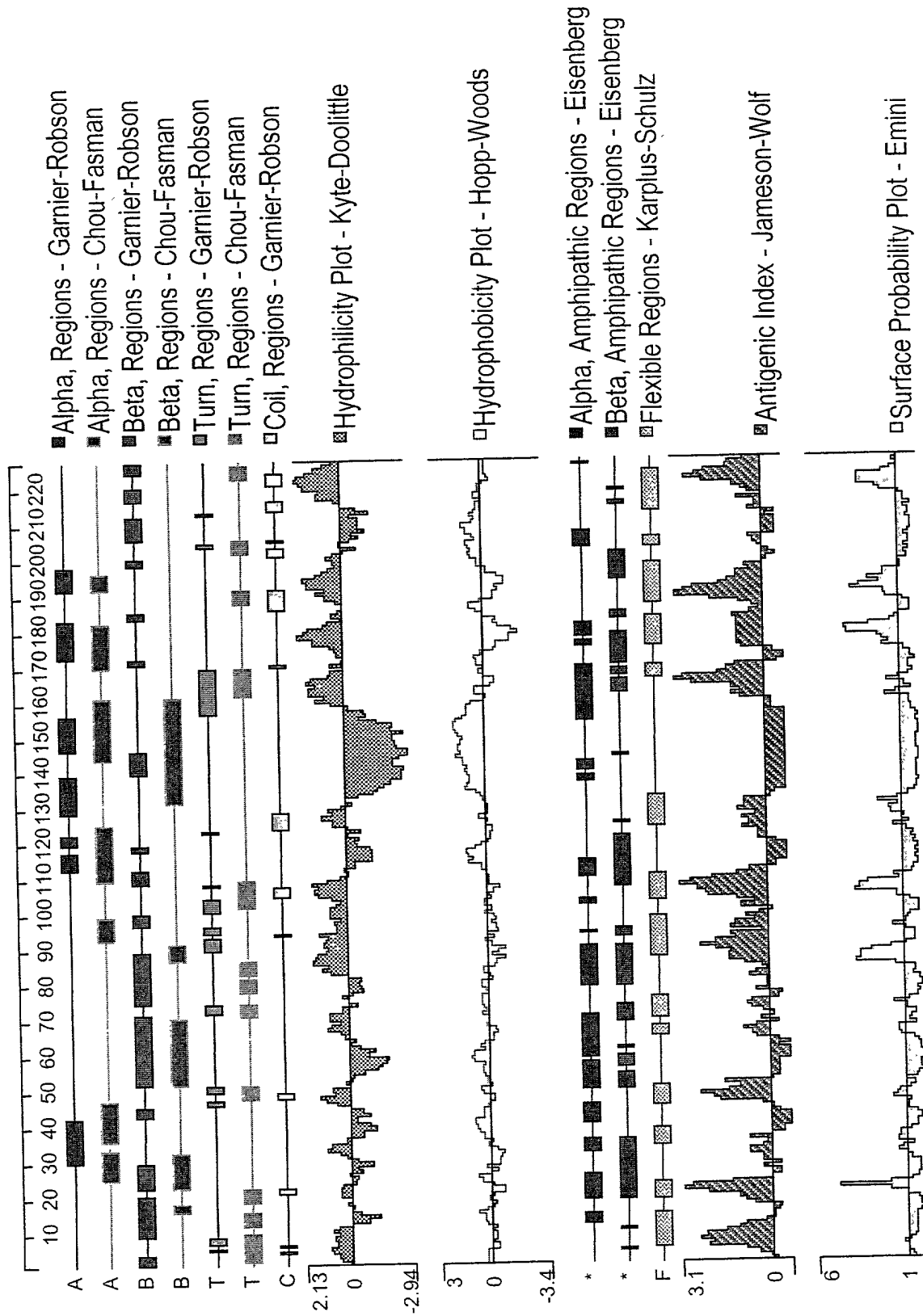


FIG. 6

1 GCAGAAGCAGCAGCCGAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 60
 1 M 1
 *****
 61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGGAAGAACTGAGAGGCGC 120
 2 A E P G H S H H L S A R V R G R T E R R 21

 121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180
 22 I P R L W R L L L W A G T A F Q V T Q G 41

 181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
 42 T G P E L H A C K E S E Y H Y E Y T A C 61
 ++++++
 241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGCCTGTGCACCAGC 300
 62 D S T G S R W R V A V P H T P G L C T S 81
 + ++++++
 301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGAGTTTCTG 360
 82 L P D P V K G T E C S F S C N A G E F L 101
 *****
 361 GATATGAAGGACCACTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 420
 102 D M K D Q S C K P C A E G R Y S L G T G 121

 421 ATTCCGTTTGTATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 480
 122 I R F D E W D E L P H G F A S L S A N M 141
+++++*****.
 481 GAGCTGGATGACAGTCTGCTGAGTCCACCGGGAAGTGTACTTCGTCCAAGTGGGTTCCTC 540
 142 E L D D S A A E S T G N C T S S K W V P 161

 541 CGGGGCGACTACATCGCCTTCAACACGGACGAATGCACAGCCCACTGATGTACGCCGTC 600
 162 R G D Y I A F N T D E C T A T L M Y A V 181

 601 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 660
 182 N L K Q S G T V N F E Y Y Y P D S S I I 201

FIG. 7A

661 TTTGAGTTTTTCGTTTCTCAGAATGACCAGTGGCCAGCCCAATGCAGATGACTCCAGGTGGATG 720
 202 F E F F V Q N D Q C Q P N A D D S R W M 221

 721 AAGACCACAGAGAAAGGATGGGAATTCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 780
 222 K T T E K G W E F H S V E L N R G N N V 241
 .
 781 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 840
 242 L Y W R T T A F S V W T K V P K P V L V 261
 .
 ++++++
 841 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 900
 262 R N I A I T G V A Y T S E C F P C K P G 281
 .
 ++++++
 901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACCTTGCCAGCCAACTCTTATTCA 960
 282 T Y A D K Q G S S F C K L C P A N S Y S 301
 .
 ***** ++++
 961 AATAAAGGAGAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020
 302 N K G E T S C H Q C D P D K Y S E K G S 321
 ++++++ *****
 1021 TCTTCCTGTAACTGCGCCAGCTTGACAGACAAAGATTATTTCTACACACACACGGCC 1080
 322 S S C N V R P A C T D K D Y F Y T H T A 341
 .
 1081 TGCGATGCCAACGGAGAGACACAACACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140
 342 C D A N G E T Q L M Y K W A K P K I C S 361
 .
 1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200
 362 E D L E G A V K L P A S G V K T H C P P 381
 .
 ++++++
 1201 TGCAACCCAGGCTTCTTCAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
 382 C N P G F F K T N N S T C Q P C P Y G S 401
 ++++++ ++++++
 1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320
 402 Y S N G S D C T R C P A G T E P A V G F 421

FIG. 7B

1321 GAATACAAATGGTGAACACGCTGCCACAAACATGGAACGACCGTTCTCAGTGGGATC 1380
 422 E Y K W W N T L P T N M E T T V L S G I 441
 1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440
 442 N F E Y K G M T C W E V A G D H I Y T A 461
 ++++++.
 1441 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGATTAGACCT 1500
 462 A G A S D N D F M I L T L V V P G F R P 481
 1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
 482 P Q S V M A D T E N K E V A R I T F V F 501
 1561 GAGACCCTCTGTTCTGTGAAGTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620
 502 E T L C S V N C E L Y F M V G V N S R T 521

 1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCCAAACAGTCCTATACCTACATCATT 1680
 522 N T P V E T W K G S K G K Q S Y T Y I I 541
 1681 GAGGAGAACTACCACGAGCTTCACCTGGGCCTTCAGAGGACCACTTTTCATGAGGCA 1740
 542 E E N T T T S F T W A F Q R T T F H E A 561

 1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
 562 S R K Y T N D V A K I Y S I N V T N V M 581
 . +++++.
 1801 AATGGCGTGGCCTCCTACTGCCGTCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860
 582 N G V A S Y C R P C A L E A S D V G S S 601
 +++++. . . . +++++.
 1861 TGCACCTCTTGCTGCTGCTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
 602 C T S C P A G Y Y I D R D S G T C H S C 621
 . +++++.
 1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980
 622 P P N T I L K A H Q P Y G V Q A C V P C 641

FIG. 7C

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1981 GGTCCAGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040
642 G P G T K N N K I H S L C Y N D C T F S 661

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2041 CGCAACACTCCAACCAGGACTTTCAACTACAATTCTCCGCTTTGGCAAACACCGTCACT 2100
662 R N T P T R T F N Y N F S A L A N T V T 681

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2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCTC 2160
682 L A G G P S F T S K G L K Y F H H F T L 701

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2161 AGTCTCTGTGGAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220
702 S L C G N Q G R K M S V C T D N V T D L 721

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2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAATCTATCACAGCCTACGTCTGCCAGGCA 2280
722 R I P E G E S G F S K S I T A Y V C Q A 741

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2281 GTCATCATCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340
742 V I I P P E V T G Y K A G V S S Q P V S 761

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2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400
762 L A D R L I G V T T D M T L D G I T S P 781

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2401 GCTGAACCTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460
782 A E L F H L E S L G I P D V I F F Y R S 801

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*****
2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520
802 N D V T Q S C S S G R S T T I R V R C S 821

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.
+++++
2521 CCACAGAAAAGTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580
822 P Q K T V P G S L L L P G T C S D G T C 841

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+++++
2581 GATGGCTGCAACTTCCACTTCTGTGGGAGAGCGGGCTGCTTGCCCGCTCTGCTCAGTG 2640
842 D G C N F H F L W E S A A A C P L C S V 861

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FIG. 7D

2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700
 862 A—D Y H A I V S S C V A G I Q K T T Y V 881
 2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTCTCTGCCTGAGCAGAGATCACCATC 2760
 882 W R E P K L C S G G I S—L—P—E Q R V T I 901
 2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820
 902 C K T I D F W L K V G I S A G T C T A I 921
 2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAAGTAGAGTACAAGTAC 2880
 922 L L T V L T C Y F W k k n q k l e y k y 941
 2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940
 942 s k l v m n a ~~t—l—k—d~~ c d l p a a d s c 961
 2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAATCACTCT 3000
 962 a i m e g e d v e d d l i f t . s k n h s 981
 3001 TTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTGACTCAGTGCCGC 3060
 982 l g r s n h l p p r g l l m d l t q c r 1001
 3061 TGAAGACATCCTCAGGAGGCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCTG 3120
 1002 * 1002
 3121 CCTCCTCACCTTGCCATAGCACCTTTGCAAGCCTGCGGCGATTGGGTGCCAGCATCCTGC 3180
 3181 AACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTCAGATCT 3240
 3241 TTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCCTCAAACCTGCCAAATATACCCA 3300
 3301 CACTTTGTTTGTAAATTAAAAA 3334

FIG. 7E

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FIG. 8A

		10	20	30	
1	MAEPGHSHHLSARVRGRTERRIPRLWRLLL	TR13-alpha.aa			
1	M-----	gb AAB94382.1 TNF Receptor II			
		40	50	60	
31	WAGTAFOVTOGTGPELHACKESYHYEYTA	TR13-alpha.aa			
2	-----KSVLYSYIL--	gb AAB94382.1 TNF Receptor II			
		70	80	90	
61	CDSTGSRWRVAVPHTPGLCTSLPDPVKGTE	TR13-alpha.aa			
11	-----	gb AAB94382.1 TNF Receptor II			
		100	110	120	
91	CSFSCNAGEFLDMKDQSCKPCAEGRYSLGT	TR13-alpha.aa			
11	-----FL-----SC-----	gb AAB94382.1 TNF Receptor II			
		130	140	150	
121	GIRFDEWDELPHGFASLSANMELDDSAAES	TR13-alpha.aa			
15	-I I I N G R D V A P Y -----A P S	gb AAB94382.1 TNF Receptor II			
		160	170	180	
151	TGNCTSSKWVPRGDYIAFNTDECTATLMYA	TR13-alpha.aa			
29	NGKCKKDNE-----	gb AAB94382.1 TNF Receptor II			
		190	200	210	
181	VNLKOSGTVNFEYYPDSSIIFEFFVQNDQ	TR13-alpha.aa			
37	-----YNRHNL	gb AAB94382.1 TNF Receptor II			
		220	230	240	
211	COPNADDSRWMKTTEKGWFEHVELNRGN	TR13-alpha.aa			
43	C-----	gb AAB94382.1 TNF Receptor II			
		250	260	270	
241	VLYWRTTAFSVWTKVPKPVLRNIAITGVA	TR13-alpha.aa			
44	-----	gb AAB94382.1 TNF Receptor II			

FIG. 8B

271	Y T S E C F P C K P G T Y A D K Q G S S F C K L C P A N S Y	TR13-alpha.aa
44	---C L S C P P G T Y A S R ---L C D S K T -	gb AAB94382.1 TNF Receptor II
301	S N K G E T S C H O C D P D K Y S E K G S S S C N V R P A C	TR13-alpha.aa
62	--N T N T Q C T P C G S D T F T S R N N H L ---P A C	gb AAB94382.1 TNF Receptor II
331	T D K D Y F Y T H T A C D A N G E T O L M Y K W A K P K I C	TR13-alpha.aa
86	---L S C N G R C D S N Q V E T R S C N T T H N R I C	gb AAB94382.1 TNF Receptor II
361	S E D L E G A V K L P A S G V K T H C P P C N P G F F K T N	TR13-alpha.aa
111	D ---C A P G Y Y ---	gb AAB94382.1 TNF Receptor II
391	N S T C O P C P Y G S Y S N G S D C T R C P A G T E P A V G	TR13-alpha.aa
118	---C L L ---K G S G C K A C V S Q T K C G I G	gb AAB94382.1 TNF Receptor II
421	F E Y K W W N T L P T N M E T T V L S G I N F E Y K G M T G	TR13-alpha.aa
138	Y ---G V S G	gb AAB94382.1 TNF Receptor II
451	W E V A G D H I Y T A A G A S D N D F M I L T L V V P G F R	TR13-alpha.aa
143	H T P T G D V I - - - - -	gb AAB94382.1 TNF Receptor II
481	P P Q S V M A D T E N K E V A R I T F V F E T L C S V N C E	TR13-alpha.aa
151	- - - - -	gb AAB94382.1 TNF Receptor II
511	L Y F M V G V N S R T N T P V E T W K G S K G K Q S Y T Y I	TR13-alpha.aa
151	- - - - -	gb AAB94382.1 TNF Receptor II

FIG. 8C

541	I E E N T T T S F T W A F O R T T F H E A S R K Y T N D V A	TR13-alpha.aa
151	-----	gb AAB94382.1 TNF Receptor II
571	K I Y S I N V T N V M N G V A S Y C R P C A L E A S D V G S	TR13-alpha.aa
151	-----C S P C G L-----	gb AAB94382.1 TNF Receptor II
601	S C T S C P A G Y Y I D R D S G T C H S C P P N T I L K A H	TR13-alpha.aa
157	-----G T Y-----S H	gb AAB94382.1 TNF Receptor II
631	O P Y G V O A C V P C G P G T K N N K I H S L C Y N D C T F	TR13-alpha.aa
162	T V S S A D K C E P-----	gb AAB94382.1 TNF Receptor II
661	S R N T P T R T F N Y N F S A L A N T V T L A G G P S F T S	TR13-alpha.aa
172	---V P S N T F N Y-----I D V E I N L-----Y P V	gb AAB94382.1 TNF Receptor II
691	K G L K Y F H H F T L S L C G N O G R K M S V C T - D N V T	TR13-alpha.aa
190	N D-----T S C T R T T T T	gb AAB94382.1 TNF Receptor II
720	D L R I P E G E S G F S K S I T A Y V C Q A V I I P P E V T	TR13-alpha.aa
201	G L S E S I S T S E L T I T M N H K D C D P V-----	gb AAB94382.1 TNF Receptor II
750	G Y K A G V S S O P V S L A D R L I G V T T D M T L D G I T	TR13-alpha.aa
224	- F R D G Y F S-----V L N K V A	gb AAB94382.1 TNF Receptor II
780	S P A E L F H L E S L G I P D V I F F Y R S N D V T Q S C S	TR13-alpha.aa
237	T S G-----F F T G E N R Y Q N T S	gb AAB94382.1 TNF Receptor II

FIG. 8D

810	SGRSTTIRVRCSPQKTVPGLLLPGTCS DG	TR13-alpha.aa
252	NVCTLNFEIKC N N K D S S S K Q L - - - - -	gb AAB94382.1 TNF Receptor II
840	TC D G C N F H F L W E S A A A C P L C S V A D Y H A I V S	TR13-alpha.aa
273	- - - - - T K T K N D T I M P H S E T V T L V G	gb AAB94382.1 TNF Receptor II
870	S C V A G I O K T T Y V W R E P K L C S G G I S L P E O R V	TR13-alpha.aa
292	D C L S S V D - - I Y I - - - - L Y S N T - - - - -	gb AAB94382.1 TNF Receptor II
900	T I C K T I D F W L K V G I S A G T C T A I L L T V L T C Y	TR13-alpha.aa
307	- - - N T Q D Y - - - - -	gb AAB94382.1 TNF Receptor II
930	F W K K N O K L E Y K Y S K L V M N A T L K D C D L P A A D	TR13-alpha.aa
312	- - - E T D T I S Y H A G N V L - - - - - D V D S H M P G	gb AAB94382.1 TNF Receptor II
960	S C A I M E G E D V E D D L I F T S K N H S L G R S N H L P	TR13-alpha.aa
333	S C D I - - - - - H K L I T N S Q N P	gb AAB94382.1 TNF Receptor II
990	P R G L L M D L T Q C R	TR13-alpha.aa
347	T H - - - - - F L	gb AAB94382.1 TNF Receptor II

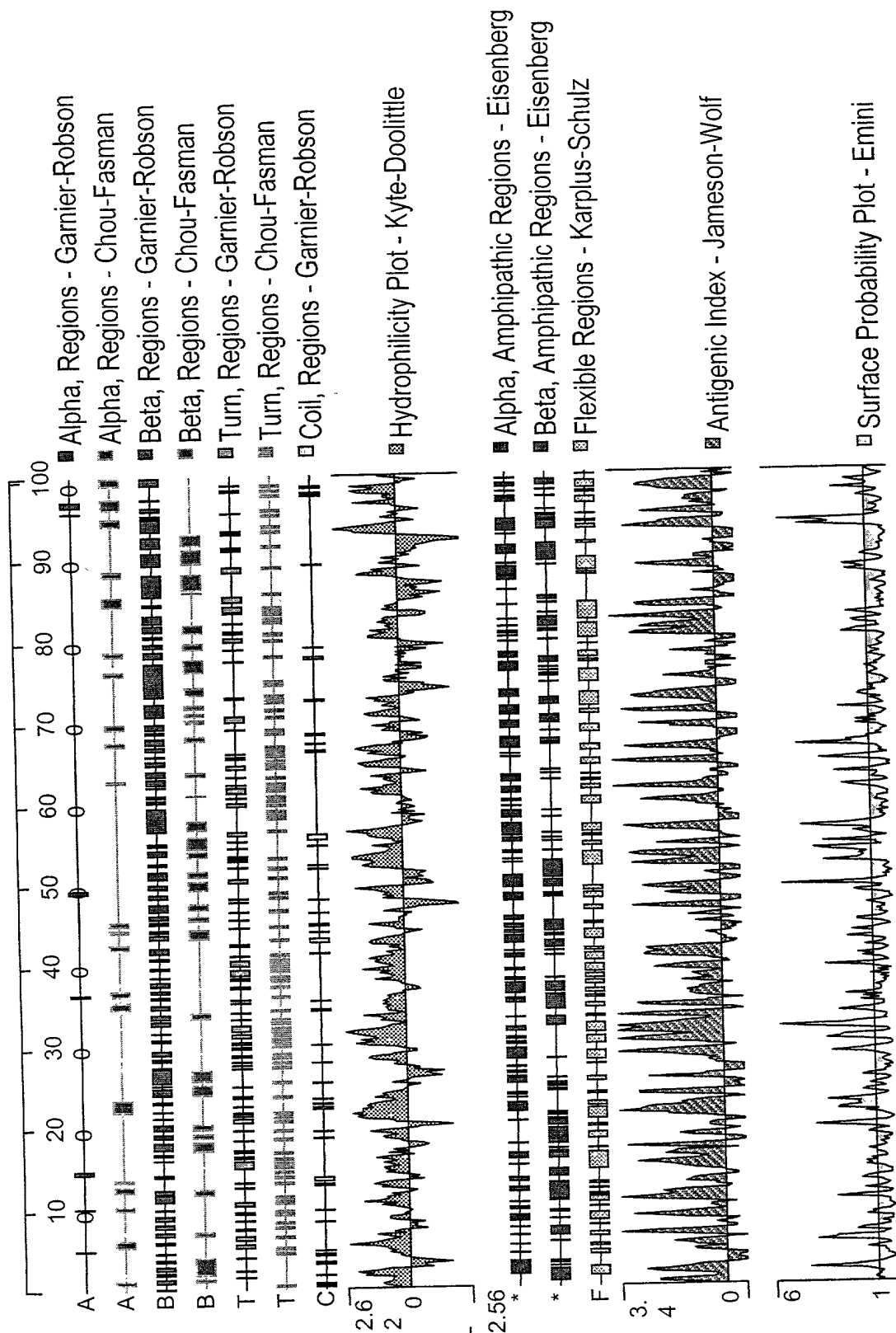


FIG. 9

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1	GGATTGTACCGGAGTCCCATTTGGGAGCAAGAGCCATCTACTCGTCCGTTACCGGCCTT	60
61	CCCACCATGGATTGCCAAGAAATGAGTACTGGGACCAATGGGACGGTGTGTCAACCTGC	120
1	M D C Q E N E Y W D Q W G R C V T C	18
121	CAACGGTGTGGTCCCTGGACAGGAGCTATCCAAGGATTGTGGTTATGGAGAGGTTGGAGAT	180
19	Q R C G P G Q E L S K D C G Y G E G D	38
181	GCCTACTGGCACAGCCTGCCCTCCTCGCAGTACAAAGCAGCTGGGGCCACCACAAATGT	240
39	A Y W H S L P S S Q Y K S S W G H H K C	58
241	CAGAGTTGCATCACCTGTGCTGTCAATCGTGTTCAGAAGGTCAACTGCACACCTACC	300
59	Q S C I T C A V I N R V Q K V N C T P T	78

FIG. 10A

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601	GAGGCTGATAAAACAGCAAGGAGGAATCTCTCTTCCCGTGCCACCCAGCAAGGAGACC	660
179	E A D K T A K E E S L F P V P P S K E T	198
661	AGTGCTGAGTCCCAAGTCTCTTGGGCCCCCTGGCAGCCTTGCCCCAGTTGTTCTCTCTGGAC	720
199	S A E S Q V S W A P G S L A Q L F S L D	218
721	TCTGTTCCTATACCACAACAGCAGCAGGGGCCCTGAAATGTGATGTCCACAAGAGCTAATA	780
219	S V P I P Q Q Q Q G P E M *	232
781	CCCTACAGATGGGGCATATCCTATCCCATCCCAACAGAGGATTGATTCCTCCATTTCACAA	840
841	GGACTGATCTGGAGCATTTCTTGCTTCCCTGTGTGTAGTCTGGGGAGCCAGATTCCACATT	900
901	CATGGGACTACCAGACATGTTCCCTAGCTCAACTTGATTATAGAGAAGAGGAGAGAGGACA	960

FIG. 10C

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961	GTGAATGGGTAGGGTTTTCATGTCCTGCAATTTTGGTCAGGTAAGCCTCTCAAAATTGTG	1020
1021	TTGGCACATCTACCTAGCACCTTTAGGGACAAATCAAAACCTTCTCCCCCTTTTAGCTCCT	1080
1081	CCACACTGCCCTCCCTCCTCAACACACACACACATACACACACATATACATAGACAC	1140
1141	ACAAACACACACACACATTAATATCTATCTTGGGGGAAGCCTCGTGCCATAATTCCCA	1200
1201	AGTCATGTCCTCAGACTGCTGCAATTCAGCATGACGAGGGCAACACTTTCCTCTAGAT	1260
1261	CCCTGGGGCCTCACCCCTGTATTTGAGGTTCTCACCACCTCAGCAGGAGAGGGCTGAA	1320
1321	GTTCCGCATTTTGGAACCTTACAGAACAATTTCTGAGCCAAAGTAATCTTCCTTCTGGGGC	1380

FIG. 10D

[illegible]

FIG. 10E

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1801 TAAGGCCCTTGGGCAACCAATTGATCAGATTACTAAAGGACTTGGGAAAAGCAAAA 1860
1861 AGTCCCATTTGTACTGGTACTGAGGATTAGAAGCAATTGAAATACAAGCCTGTACCAAGC 1920
1921 AAGCAGCCTGGCCCCACACAGGTATTAGCAAATAATGTGGTAACCAAGTTTTAGGCCTTG 1980
1981 GSCYCTAGGTTCCCTGTTTTTTTTCGTTTGGTTTCCGTTTTCGTTTTTTTGCAACAGGT 2040
2041 TATTCTTATCTCACTGGCTTTCACCTGATCATGTTTAGACCTTCTGTAGAGAAATAATA 2100
2101 TCCAGACAGGGGATGATTGGCTTCAGCAGGCTGCAGGTGTTCAAAGTTGCCATGTGGC 2160
2161 TGGCAGTGGTTCAAGCCCACATTTGACACTGCTGCTCTAGAGGAAAGATAATGATGGTAA 2220

FIG. 10F

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2221 CACAGTAATAATAATAAATAAATAAATAAAGTGAAGAGTAGATTCTTTCA 2280
2281 GTGTGCTTGCTCCATGGCATGAATGCTATGTGGACAGCCCAAGCCATACCCAGAAATCACC 2340
2341 TTAATTCCAACCTTTTGAGGTTTCAGCAATTGGAGGTGGCAATTGGCTTTGCATTTTAAAG 2400
2401 TATTTCCGGTAAAGTGAAGTGAAGGATTTTCGCTCTTTAATAATTCTGTTTGGCCATGGC 2460
2461 AAATACCATAGTTGAGTATTTGCTTCAGGAGAGTTCTTTTACAGTTTACTTTTCAATG 2520
2521 CTGAGGCATATTTCTTTGAGCACCTGTGCTTTTATGTGCTCTTCTACAAGGGTTATTGG 2580
2581 TCAGTGAAGAACAAAGTACACTTGATAAAAAACATTTTCAACATACATTGAGCCTAAACA 2640
2641 GCAGTTAAGTTGTCTCTAATGAAGTACCAAAAAAATAATGTAGTTTGTGTTGTAAGG 2700

FIG. 10G

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2701	AAGGGAGGTATTCTCTGAGATGAATTTT	TTT	TTT	TGGATTACTGTTT	CTCTCCA	2760	
2761	TATACCTTGAAC	TGGGATTT	GAA	CAGGAGGAAGT	CCTGGGAAAAATAATTT	TTTCCC	2820
2821	TCCAAGATTCTCAGATCC	CAGGTTAGGA	AAGGATTCAGC	ACTAACAGCATA	ACCCCTCTA	2880	
2881	CAACATACAGCCCTGTCACAT	TGAGATCATAAT	CCCTCCTGT	CCCAC	TCTCTACCAA	2940	
2941	CCCCACCTACTAGCTAGG	CTTCAGTGT	TTTACATTTGA	ATATGGTACATTT	TAATAT	3000	
3001	TTTTTCTCATAAA	TGGGTTATTT	TATAGAGATTT	TGTAACTCTTGAGCC	TATGCATGTG	3060	
3061	TAGATACTGGCAGG	CTATGTTGT	TTATGATGCTCTGCA	AACATTT	CATATTTGGCCAAT	3120	
3121	AAACAGAAATATAT	CCAAAA	AAAA	AAAA	AAAA	3152	

FIG. 10H

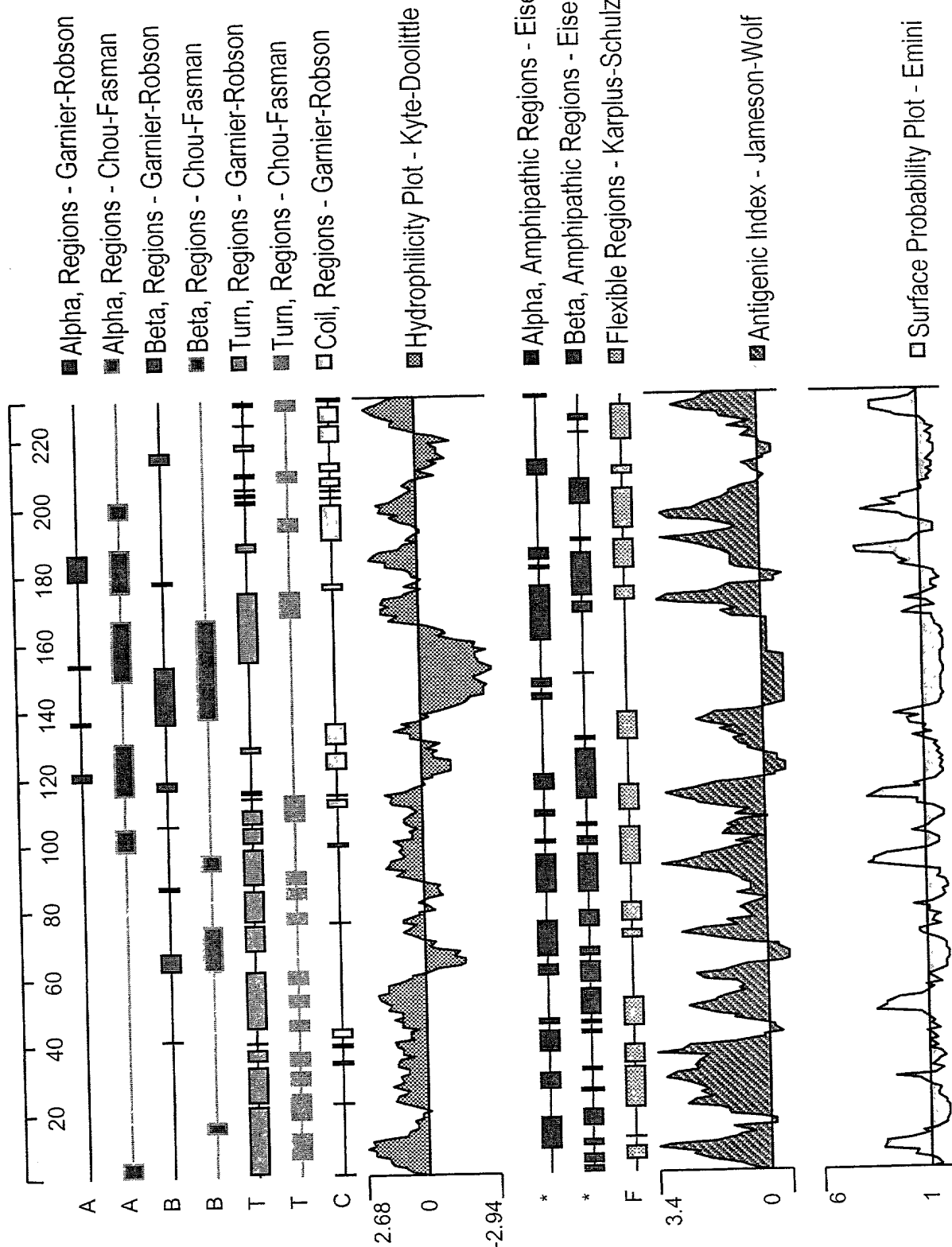


FIG. 11

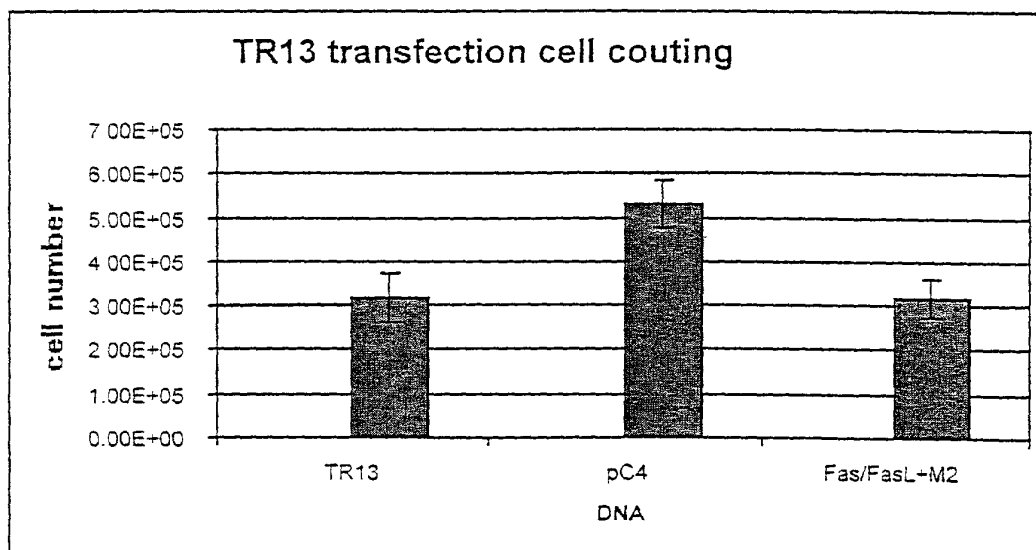


FIG. 12